SEQUENCE LISTING

<110> Walke, D. Wade
      Wilganowski, Nathaniel
      Turner, C. Alexander Jr.
      Friedrich, Glenn
      Abuin, Alejandro
      Zambrowicz, Brian
      Sands, Arthur T.

<120> Novel Human Membrane Protein and
   Polynucleotides Encoding the Same

<130> LEX-0115-USA

<150> US 60/175,764
<151> 2000-01-12

<160> 3

<170> FastSEQ for Windows Version 4.0

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<212> DNA
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caaccacctt cgcccagctc caaggaccaa ggaaagatgg tttctctctt ctatggaatc   840
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<212> PRT
<213> Homo Sapien

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            20   25   30

1

Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
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Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
        50   55   60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
65   70   75   80
Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
                85   90   95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
                100   105   110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
        115   120   125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
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Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
145   150   155   160
Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
                165   170   175
Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
                180   185   190
Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
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Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
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Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225   230   235   240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
                245   250   255
Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
                260   265   270
Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
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<212> DNA
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gaaatagtta acaaatatgt gttaattgac ttcctgaatt tttctgtttc aggaaaccaa   180
gagttgaaac attaatcatg aattgggtaa atgacagcat catacaggag tttattctgc   240
tgggtttctc agatcgacct tggctggagt ttccactcct tgtggtcttc ttgatttctt   300
acactgtgac catctttggc aatctgacca ttattctagt gtcacgcctg acaccaaac   360
ttcatacccc catgtatttt tttcttacca atctatcact cctggatctt tgttacacca   420
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ccgtctctgt gtacctgcaa ccaccttcgc ccagctccaa ggaccaagga aagatggttt     1020
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aggaggtaaa ggaaggcttt aaaaggttgg ttgcaagagt cttcttaatc aagaaataag     1140
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tttccttgat gaagagctat atttacttct gttgccttaa tgttttcatt gaacaagccc     1320
ccagaattga ccttccaatt caccaaaaat tgtaatcaca acatcttcaa ggtttgtcaa     1380
acatcccatc aatgcttgta caattcaatg taaattagat ccgtagaaaa gccagaagtt     1440
ctttctccaa tatcacacac acacacacac acacacacac acacac                    1488
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